

**AMENDMENTS TO THE SPECIFICATION**

Please replace the title of application recited at page 1, lines 1-3 with the following title.

Method of Promoting Stem Cell Proliferation or Survival by Contacting a Cell with a Novel Stem Cell Factor-Like Polypeptide.

Please replace the paragraph beginning at page 1, line 6 with the following amended paragraph.

This application claims priority of U.S. Provisional Application Serial No. 60/282,397 filed April 5, 2001, and U.S. Provisional Application Serial No. 60/215,733, filed June 28, 2000, and U.S. Provisional Application Serial No. 60/266,614 filed February 5, 2001, Attorney Docket No. 21272-039, is a continuation-in-part application of U.S. Application Serial No. 09/757,562 filed January 09, 2001, now abandoned, entitled "Methods and Materials Relating to Novel Stem Cell Growth Factor-Like Polypeptides and Polynucleotides", Attorney Docket No. HYS-4CON; which in turn is a continuation application of U.S. Application Serial No. 09/543,774 filed April 5, 2000, now abandoned, entitled "Methods and Materials Relating to Novel Stem Cell Growth Factor-Like Polypeptides and Polynucleotides", Attorney Docket No. HYS-4; which in turn is a continuation-in-part application of U.S. Application Serial No. 09/496,914 filed February 03, 2000, now abandoned, entitled "Novel Contigs Obtained from Various Libraries", Attorney Docket No. 787; all of which are incorporated herein by reference in their entirety.

Please replace the paragraph beginning at page 12, line 15 with the following amended paragraph.

Optionally preferred are polynucleotides and polypeptides other than the nucleotide sequence set forth as SEQ ID NO: 3284 (and the polypeptide sequence encoded therein) in U.S. application serial no. 09/496,914 filed February 3, 2000, now abandoned, and the protein set out in Genbank Accession No. BAB28811.

Please replace the paragraph beginning at page 165, line 18 with the following amended paragraph.

The predicted amino acid sequence for SEQ ID NO: 8 was obtained by using a software program called FASTY (available from ~~http://fasta.bioch.virginia.edu~~ at the University of Virginia web site) which selects a polypeptide based on a comparison of translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), incorporated herein by reference).

Please replace the paragraph beginning at page 173, line 7 with the following amended paragraph.

Stromal cell strain AGM-s3 derived ~~form~~ from AGM ~~which~~ was subcultured in MEM $\alpha$  medium (GIBCO BRL), including non-active 10% FCS (bovine fetal serum, Hyclone) and was suspended in PBS containing 5% FCS (PBS-FCS). Clone sorting was performed in a 96-well culture dish (Falcon) at one cell/ well using a cell sorter (FACS Vantage; Becton Dickinson). Among cells in the 96 wells, cultures of the cells which proliferated were expanded, so that thirteen kinds of AGM-s3 subclones were obtained. The activity to support the hematopoietic cells of these AGM-s3 subclones ~~were~~ was assessed.

Please replace the paragraph beginning at page 183, line 6 with the following amended paragraph.

An amplified fragment was digested with restriction enzymes EcoRI and XhoI. After electrophoresis, a DNA fragment was purified using JETSORB (Genomed, Germany). The purified DNA fragment was ligated with pMX-IRES-GFP vector digested with EcoRI and XhoI (gift ~~form~~ from Professor T. Kitamura, TOKYO UNIV. INST. OF MEDICAL SCIENCE, Japan). The pMX-IRES-GFP vector was a plasmid in which IRES GFP was inserted into the retrovirus vector pMX. The obtained recombinant vector was transferred into E. coli DH5a, and was seeded on LB agar medium containing 100 mg/ml of ampicillin, so that independent colonies ~~were~~ formed. After the isolated colony was cultured in 100 mL of LB medium containing 100 mg/ml of ampicillin, plasmid was purified using QIAGENtip100 (QIAGEN, U.S.A.). The sequence of the inserted gene was determined

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using conventional method, so that the sequence was confirmed to be identical to the corresponding region in SEQ ID NO: 31.